

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/826812  
Source: IFW  
Date Processed by STIC: 11-30-14

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 11/30/2004

PATENT APPLICATION: US/10/826,812

TIME: 15:30:15

Input Set : N:\Crf3\RULE60\10826812.raw

Output Set: N:\CRF4\11302004\J826812.raw

## SEQUENCE LISTING

## 1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Goodman, Corey S.

3 Kidd, Thomas

4 Mitchell, Kevin

5 Tear, Guy

6 (ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and  
7 Nucleic Acids

8 (iii) NUMBER OF SEQUENCES: 13

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: SCIENCE &amp; TECHNOLOGY LAW GROUP

11 (B) STREET: 75 DENISE DRIVE

12 (C) CITY: HILLSBOROUGH

13 (D) STATE: CALIFORNIA

14 (E) COUNTRY: USA

15 (F) ZIP: 94010

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Floppy disk

18 (B) COMPUTER: IBM PC compatible

19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

21 (vi) CURRENT APPLICATION DATA:

C--&gt; 22 (A) APPLICATION NUMBER: US/10/826,812

C--&gt; 23 (B) FILING DATE: 16-Apr-2004

W--&gt; 24 (C) CLASSIFICATION:

25 (vii) PRIOR APPLICATION DATA:

26 (A) APPLICATION NUMBER: US/08/971,172

27 (B) FILING DATE: 14-Nov-1997

28 (viii) ATTORNEY/AGENT INFORMATION:

29 (A) NAME: OSMAN, RICHARD A

30 (B) REGISTRATION NUMBER: 36,627

31 (C) REFERENCE/DOCKET NUMBER: B98-006

32 (ix) TELECOMMUNICATION INFORMATION:

33 (A) TELEPHONE: (650) 343-4341

34 (B) TELEFAX: (650) 343-4342

35 (2) INFORMATION FOR SEQ ID NO: 1:

36 (i) SEQUENCE CHARACTERISTICS:

37 (A) LENGTH: 4188 base pairs

38 (B) TYPE: nucleic acid

39 (C) STRANDEDNESS: double

40 (D) TOPOLOGY: linear

41 (ii) MOLECULE TYPE: cDNA

42 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Input Set : N:\Crif3\RULE60\10826812.raw

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46	ATGCATCCCA	TGCATCCCGA	AAACCACGCC	ATCGCCCGGA	GCACGAGCAC	CACTAATAAC	60
47	CCATCTCGCA	GTCGGAGCAG	CAGGATGTGG	CTCCTGCCCG	CCTGGCTGCT	CCTCGTCCTG	120
48	GTGGCCAGCA	ATGGCCTGCC	AGCAGTCAGA	GGCCAGTACC	AATCGCCACG	TATCATCGAG	180
49	CATCCCACGG	ATCTGGTCGT	TAAGAAGAAT	GAACCCGCCA	CGCTCAACTG	CAAAGTGGAG	240
50	GGCAAGCCGG	AACCCACCAT	TGAGTGGTTT	AAGGATGGCG	AACCCGTCAG	CACCAACGAA	300
51	AAGAAATCGC	ACCGCTCCA	GTTCAAGGAC	GGCGCCCTCT	TCTTTTACAG	GACAATGCAA	360
52	GGCAAGAAGG	AGCAGGACGG	CGGAGAGTAC	TGGTGCCTGG	CCAAGAACCG	AGTGGGCCAG	420
53	GCCGTTAGTC	GCCATGCCTC	CCTCCAGATA	GCTGTTTGGC	GCGACGATTT	TCGCGTGGAG	480
54	CCCAAAGACA	CGCGAGTGGC	CAAAGGCGAG	ACGGCTCTGC	TGGAGTGTGG	GCCGCCCAAA	540
55	GGCATTCCAG	AGCCAACGCT	GATTTGGATA	AAGGACGGCG	TTCCCTTGGA	CGACCTGAAA	600
56	GCCATGTCGT	TTGGCGCCAG	CTCCCGCGTT	CGAATTGTGG	ACGGTGGCAA	CCTGCTGATC	660
57	AGCAATGTGG	AGCCCATTTA	TGAGGGCAAC	TACAAGTGCA	TTGCCAGAA	TCTGGTAGGC	720
58	ACCCGCGAGA	GCAGCTATGC	CAAGCTGATT	GTCCAGGTCA	AACCATACTT	TATGAAGGAG	780
59	CCCAAGGATC	AGGTGATGCT	CTACGGCCAG	ACAGCCACTT	TCCACTGCTC	AGTGGGCGGT	840
60	GATCCGCCGC	CGAAAGTGTT	GTGGAAAAAG	GAGGAGGGCA	ATATTCCGGT	GTCCAGAGCG	900
61	CGAATCCTTC	ACGACGAGAA	AAGTTTAGAG	ATATCCAACA	TAACGCCCAC	CGATGAGGGC	960
62	ACCTATGTCT	GCGAGGCACA	CAACAATGTC	GGTCAGATCA	GCGCTAGGGC	TTCTCTTATA	1020
63	GTCCACGCTC	CGCCGAACCT	TACGAAAAGA	CCCAGTAACA	AGAAAGTGGG	ACTAAATGGG	1080
64	GTTGTCCAAC	TACCTTGCAT	GGCCTCCGGA	AACCTCCGC	CGTCTGTATT	CTGGACCAAG	1140
65	GAAGGAGTAT	CCACTCTTAT	GTTCCCAAAT	AGTTCGCACG	GAAGGCAGTA	TGTGGCTGCC	1200
66	GATGGAACTC	TGCAGATTAC	GGATGTGCGG	CAGGAAGACG	AAGGCTACTA	TGTGTGTTCC	1260
67	GCTTTCAGTG	TAGTCGATTC	CTCTACAGTA	CGGGTTTTC	TGCAAGTCAG	CTCGGTAGAC	1320
68	GAGCGTCCAC	CTCCGATTAT	TCAAATCGGA	CCTGCCAATC	AAACACTGCC	CAAGGGATCA	1380
69	GTTGCTACTT	TACCCTGTCT	GGCCACTGGA	AATCCCAGTC	CCCGTATCAA	GTGGTTCCAC	1440
70	GATGGACATG	CCGTACAAGC	GGGCAATCGA	TACAGCATCA	TCCAAGGAAG	CTCACTGAGA	1500
71	GTCGATGACC	TTCAACTAAG	TGACTCTGGT	ACCTACACCT	GCACTGCATC	TGGCGAACGA	1560
72	GGAGAAACTT	CCTGGGCTGC	CACACTAACG	GTGGAAAAAC	CCGGTTCTAC	ATCTCTTCAC	1620
73	CGGGCAGCTG	ATCCTAGCAC	TTATCCTGCT	CCTCCAGGAA	CACCTAAAGT	CCTGAATGTC	1680
74	AGTCGCACCA	GCATTAGTCT	TCGTTGGGCT	AAAAGCCAAG	AGAAACCCGG	AGCTGTGGGC	1740
75	CCAATCATTG	GATACACTGT	AGAGTACTTC	AGTCCGGATC	TGCAAACTGG	TTGGATTGTG	1800
76	GCTGCCCATC	GAGTCGGCGA	CACTCAAGTC	ACTATCTCGG	GTCTCACTCC	TGGCACTTCG	1860
77	TATGTGTTCC	TAGTTAGAGC	TGAGAATACT	CAGGGTATTT	CTGTGCCTTC	CGGCTTATCA	1920
78	AATGTTATTA	AAACCATTGA	GGCAGATTTT	GATGCAGCTT	CTGCCAATGA	TTTGTACGCA	1980
79	GCTCGAACTT	TGCTGACAGG	AAAGTCGGTG	GAGCTAATAG	ATGCCTCGGC	TATCAATGCT	2040
80	AGTGCCGTTA	GACTTGAGTG	GATGCTCCAC	GTGAGCGCTG	ATGAGAAATA	CGTAGAGGGC	2100
81	CTGCGCATA	ACTATAAGGA	TGCCAGTGTA	CCATCCGCAC	AGTATCACTC	GATCACTGTT	2160
82	ATGGATGCCT	CTGCAGAAATC	GTTTGTGGTG	GGAAACCTTA	AGAAGTACAC	CAAGTATGAG	2220
83	TTCTTCTTAA	CACCCTTTTT	TGAGACAATT	GAAGGACAGC	CCAGTAACTC	CAAGACAGCC	2280
84	CTCACCTATG	AAGATGTTCC	CTCCGCACCA	CCGGATAACA	TTCAGATTGG	CATGTACAAC	2340
85	CAAACAGCCG	GTTGGGTGCG	TTGGACTCCG	CCACCTCCC	AGCACCACAA	TGGCAATTTG	2400
86	TATGGCTACA	AGATTGAGGT	CAGCGCCGGT	AACACCATGA	AGGTGCTGGC	CAATATGACT	2460
87	CTTAATGCTA	CCACCACATC	TGTGCTCCTA	AATAACCTAA	CCACCGGAGC	TGTGTACAGC	2520
88	GTGAGTTGA	ACTCCTTTAC	CAAGGCAGGA	GATGGACCTT	ACTCCAAACC	GATATCACTA	2580
89	TTCATGGACC	CCACCCATCA	TGTGCATCCG	CCACGGGCAC	ATCCAAGCGG	CACCCATGAT	2640
90	GGGCGACATG	AGGGACAGGA	TCTCACGTAT	CATAACAATG	GCAACATAAC	ACCTGGCGAC	2700
91	ATTAATCCCA	CCACTCATAA	AAAGACCACT	GACTACCTAT	CTGGACCGTG	GCTAATGGTG	2760
92	CTGGTCTGCA	TCGTTCTTCT	AGTCCTGGTT	ATTTCCGGCG	CTATTTTCGAT	GGTCTACTTC	2820
93	AAGCGCAAGC	ATCAAATGAC	CAAGGAATTG	GGTCACTTAA	GTGTGGTCAG	TGACAAACGAA	2880
94	ATAACCGCAT	TAAATATCAA	TAGCAAAGAG	AGCCTTTTGA	TAGACCATCA	TCGTGGATGG	2940

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95   CGAACTGCCG ATACTGACAA AGACTCAGGA TTAAGCGAAT CGAAGCTACT ATCCCACGTT 3000
96   AACAGCAGTC AATCCAAC TAATAACTCC GATGGAGGAA CCGATTATGC AGAAGTTGAC 3060
97   ACCCGTAACC TTACCACCTT CTACAATTGT CGCAAGAGCC CCGATAATCC CACGCCGTAC 3120
98   GCCACCACTA TGATCATTTG TACCTCTTCC AGTGAGACCT GCACCAAGAC AACATCTATA 3180
99   AGTGCCGATA AGGACTCGGG AACTCATTCG CCCTATTCTG ACGCATTTCG CGGTTCAGGTG 3240
100  CCAGCGGTTT CTGTTGTCAA ATCCAACAT CTTAGTATC CGTTTGAACC GATCAACTGG 3300
101  TCAGAGTTTC TACCCCGGCC GCCAGAACAC CCACCTCCGT CTTCTACCTA TGGATACGCA 3360
102  CAAGGATCTC CTGAATCTTC GCGGAAGAGC TCCAAAAGCG CAGGTTCCGG CATTTCTACA 3420
103  AATCAAAGCA TTCTGAACGC ATCCATACAC AGCAGCTCCT CGGGCGGCTT TTCAGCTTGG 3480
104  GGAGTATCGC CCCAATATGC TGTCGCCTGT CCACCGGAAA ACGTTTATAG CAATCCGCTG 3540
105  TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCACAAA CCAACATCCG 3600
106  CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC 3660
107  CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG 3720
108  CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCGATGCCT TGGCCACACC CTCGCCCATG 3780
109  CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCAGTGCA TCCCAATAGC 3840
110  CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG 3900
111  GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC 3960
112  AGTGCCAAAC AACGCGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG 4020
113  GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC 4080
114  TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC 4140
115  GAGGCGGGCG AGCCGCGGCC TCGTCAAATG ACTGCTAAGA ACACCTAA 4188

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## 117 (2) INFORMATION FOR SEQ ID NO: 2:

## 118 (i) SEQUENCE CHARACTERISTICS:

119 (A) LENGTH: 1395 amino acids

120 (B) TYPE: amino acid

121 (C) STRANDEDNESS: single

122 (D) TOPOLOGY: linear

## 123 (ii) MOLECULE TYPE: peptide

## 124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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125   Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
126   1           5           10           15
127   Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Arg Met Trp Leu Leu
128   20           25           30
129   Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
130   35           40           45
131   Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
132   50           55           60
133   Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
134   65           70           75           80
135   Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
136   85           90           95
137   Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
138   100          105          110
139   Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
140   115          120          125
141   Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
142   130          135          140
143   His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
144   145          150          155          160

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145   Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
146                               165                               170                               175
147   Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
148                               180                               185                               190
149   Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
150                               195                               200                               205
151   Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
152                               210                               215                               220
153   Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
154   225                               230                               235                               240
155   Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
156                               245                               250                               255
157   Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
158                               260                               265                               270
159   Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp
160                               275                               280                               285
161   Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
162   290                               295                               300
163   Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
164   305                               310                               315                               320
165   Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
166                               325                               330                               335
167   Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
168                               340                               345                               350
169   Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
170   355                               360                               365
171   Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
172   370                               375                               380
173   Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
174   385                               390                               395                               400
175   Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
176   405                               410                               415
177   Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
178   420                               425                               430
179   Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
180   435                               440                               445
181   Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
182   450                               455                               460
183   Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
184   465                               470                               475                               480
185   Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
186   485                               490                               495
187   Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
188   500                               505                               510
189   Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
190   515                               520                               525
191   Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
192   530                               535                               540
193   Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val

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Input Set : N:\CrF3\RULE60\10826812.raw

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194	545	550	555	560
195	Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro			
196		565	570	575
197	Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro			
198		580	585	590
199	Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr			
200		595	600	605
201	Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu			
202		610	615	620
203	Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser			
204		625	630	635
205	Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn			
206		645	650	655
207	Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu			
208		660	665	670
209	Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met			
210		675	680	685
211	Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His			
212		690	695	700
213	Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val			
214		705	710	715
215	Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr			
216		725	730	735
217	Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly			
218		740	745	750
219	Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser			
220		755	760	765
221	Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly			
222		770	775	780
223	Trp Val Arg Trp Thr Pro Pro Pro Ser Gln His His Asn Gly Asn Leu			
224		785	790	795
225	Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu			
226		805	810	815
227	Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn			
228		820	825	830
229	Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys			
230		835	840	845
231	Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro			
232		850	855	860
233	Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp			
234		865	870	875
235	Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile			
236		885	890	895
237	Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr			
238		900	905	910
239	Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val			
240		915	920	925
241	Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His			
242		930	935	940

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/826,812

DATE: 11/30/2004  
TIME: 15:30:16

Input Set : N:\Crf3\RULE60\10826812.raw  
Output Set: N:\CRF4\11302004\J826812.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 855,1186  
Seq#:10; Xaa Pos.285,396

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/826,812

DATE: 11/30/2004

TIME: 15:30:16

Input Set : N:\Crf3\RULE60\10826812.raw

Output Set: N:\CRF4\11302004\J826812.raw

L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:29 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)  
L:1200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:272  
M:341 Repeated in SeqNo=10